

EXHIBIT A

Alignment of amino acid sequences of glutaminases

		1	50
gls (2247)	(1)	MVAFESLWPQNLSCTRVYSAKEIISLDSMLTMTPIPEYLHEILDVDRDITS	
GLSA_CORGL	(1)	-----	-----
GLSA_COREF	(1)	-----	-----
GLSA1_BRAJA	(1)	-----	-----
GLSA2_BRAJA	(1)	-----	-----
GLSA_ANASP	(1)	-----	-----
Consensus	(1)	MS SA MLTMTPIPEYL EILDVDRDITS	
		51	100
gls (2247)	(51)	GELADYIPELKSADPNPLAVALCTVNGHIYSAGDDDEFTMQSISKPFAY	
GLSA_CORGL	(23)	GELADYIPELKSADPNPLAVALCTVNGHIYSAGDDDEFTMQSISKPFAY	
GLSA_COREF	(27)	GEVAGYIPELKSADPNPLAVALCTVNGHIYSAGDDDEFTMQSISKPFAY	
GLSA1_BRAJA	(33)	GAVADYIPELGNADPAYFGISLATEOGHIVYVGDSTRVPTIQSMKSPFV	
GLSA2_BRAJA	(43)	GELADYIPELKRANPDHFGIALVTUOGHIVYVGDSTRVPTIQSMKAFV	
GLSA_ANASP	(34)	GIVANYIPELAKVNPDLFSISITVVGQVYVGDYQQLFTIQSISKVFAY	
Consensus	(51)	GELADYIPELK ADPNPLAVALCTVNGHIY VGDDEFTMQSISKPFAY	
		101	150
gls (2247)	(101)	ALALQECGFDEVSAVALGPSGEAFNELSLDG-ENRPMNPMINAGATAIN	
GLSA_CORGL	(73)	ALALQECGFDEVSAVALGPSGEAFNELSLDG-ENRPMNPMINAGATAIN	
GLSA_COREF	(77)	ALALQECGFDEVSAVALGPSGEAFNELSLDGSTNRPMNPMINAGATAIN	
GLSA1_BRAJA	(83)	ALALDLCAGRVESATGVPSGDPFNSIRLNSDN-HPNPMVNAGATACT	
GLSA2_BRAJA	(93)	ALALETVGEERVSATIGVPSGEAFNSIRLINDN-RPNPMVNAGATACT	
GLSA_ANASP	(84)	GLALEDHGROYVLTGVGEPTGEAFNATIEDEQSKRPYNPMVNAGATACT	
Consensus	(101)	ALALQE G DRVSASVGLGPSGEAFNELSLDG NRPMNPMINAGATAIN	
		151	200
gls (2247)	(150)	QLINGSDSTVEDRVEKIRYFSELAGRELITDRVLAESLACADRNLSIA	
GLSA_CORGL	(122)	QLINGSDSTVEDRVEKIRYFSELAGRELITDRVLAESLACADRNLSIA	
GLSA_COREF	(127)	QLINGSESSVEDRVEKIRSYFSELAGRELINDROSETEIEGADRNLSIA	
GLSA1_BRAJA	(132)	GLIYDSXG-ALAEFOIRLALSRAFGRDLAVDEAVSSSOTGDRNRATIG	
GLSA2_BRAJA	(142)	GLIYEDVG-KGAFERVRSLSEFAGRELGVDEAVHASETATGNRNRATIA	
GLSA_ANASP	(134)	SLIKGAG-TERLNVLNEMRYTIGDVFQDISVFTSERSTGHRNRAMA	
Consensus	(151)	QLINGSDSTVEDRVEKIRYFSELAGRELITDRVLAESLACADRNLSIA	
		201	250
gls (2247)	(200)	HMLRNYGVIEDAHDAVLSYTLQCAIKVTIRDLAVMTATLAAGGTHPIIG	
GLSA_CORGL	(172)	HMLRNYGVIEDAHDAVLSYTLQCAIKVTIRDLAVMTATLAAGGTHPIIG	
GLSA_COREF	(177)	HMLRNYGVIEDAHDAVLSYTLQCSVKVTARDLAVMTATLAAGGTHPIIG	
GLSA1_BRAJA	(180)	YLLKTNVAVISDNVAIVEDVYFROCAVLTARDLAVMAATLANRGINPVTG	
GLSA2_BRAJA	(190)	HMLRNYAVLPDVEDVAVEDVYFROCAVLTARDLAVMAATLANRGINPVTG	
GLSA_ANASP	(182)	HMLNFGMIDRNIIEAEDLYFGQCAVMVNHDLAVMAATLANRGVNPVTG	
Consensus	(201)	HLLRNYGVIEDAHDAVLSYTLQCAIKVTARDLAVMTATLANRGTPNITG	
		251	300
gls (2247)	(250)	KKLEDARVCRILTSMASAGMYDEAGQWLSVVGIPAKSGVAGGLIGILPG	
GLSA_CORGL	(222)	KKLEDARVCRILTSMASAGMYDEAGQWLSVVGIPAKSGVAGGLIGILPG	
GLSA_COREF	(227)	EKLVDARVAREVLTSMASAGMYDEAGQWLTAVGIPAKSGVSGGLVGVLP	
GLSA1_BRAJA	(230)	EDVNSAYATSRILTSMVTSSGMYDYAGEHTYRIGIPAKSGVGGGLAALPA	
GLSA2_BRAJA	(240)	AOVITPHIVARTLSVMTSSGMYDYAGEHTYRIGIPAKSGVGGGLAALPS	
GLSA_ANASP	(232)	EOAVNSRYIKDILTSMVTCGMYNFAGWYKVGIPAKSGVCCGIMAVVNP	
Consensus	(251)	EQLLDARVIRLTLSMASAGMYDEAGQWLYVVGIPAKSGVAGGIIATLPG	
		301	350
gls (2247)	(300)	QLGATFSPRLNPKGNSVRGVKIFKQLSDDMGLHLMSTEQVSGHAVRSIT	
GLSA_CORGL	(272)	QLGATFSPRLNPKGNSVRGVKIFKQLSDDMGLHLMSTEQVSGHAVRSIT	
GLSA_COREF	(277)	QLGATFSPRLNSGPNVRGVEIFKALSEDMLHLMSEALTOHAVRAIE	
GLSA1_BRAJA	(280)	RLGLGSYSPKLDKHGNSVRGKYCEALSSHYDLHMLNRSDDARNAVIADY	
GLSA2_BRAJA	(290)	QLGEGTFSPILDNHFNNSVRGLKYCEALSARFDLHMLNRNADVRTSMADY	
GLSA_ANASP	(282)	LMGHAVFSPPDIDRGNSVRGVKICEELSQQLGLHFECKVGNGEWGVGN	
Consensus	(301)	QLGATFSPRLN KGNNSVRGVKIFKALSDDMGLHLMSE VS HAVRAI	
		351	400
gls (2247)	(350)	RDG-----DTTFIQMGAMNFSASESEFLHAIIVH	
GLSA_CORGL	(322)	RDG-----DTTFIQMGAMNFSASESEFLHAIIVH	
GLSA_COREF	(327)	ERG-----DTTFIQMGAMNFSASESEFLHAIIVH	
GLSA1_BRAJA	(330)	DIGKSPSRRVRRAQEREILAAHEQVRNIELVGTISLSAVDYVSRRVAGR	

GLSA2_BRAJA	(340)	DVYGISSRRSROPHEQOILDERHSDIRIVELVGAINEGTIDYVTRRTSE	
GLSA_ANASP	(332)	CEC-----	
Consensus	(351)	DDG-----DTTIIQLQGAMNFSASE FL I EH	
		401-----450	
gls (2247)	(379)	NFEGTEVVLDTIRVLSFHPVAIRMKEGLKRIRDAGFEVFILOPDDVLPD	
GLSA_CORGL	(351)	NFEGTEVVLDTIRVLSFHPVAIRMKEGLKRIRDAGFEVFILOPDDVLPD	
GLSA_COREF	(356)	DFTGEKVVLDTIRVLSFHPVAIRMKEGLKRIRDAGFEVFILOPDDVLPD	
GLSA1_BRAJA	(380)	P-RPQFVTFDLIRVISTTRAGARLVAFEEELAALNVTVESGVRRASKE	
GLSA2_BRAJA	(390)	PPNAPLESDIDFRFVPDITAAGAELEGITATAGNAVVTIISGLEASAV	
GLSA_ANASP	(335)	-----	
Consensus	(401)	F G VVLDLTRV SF PVG RLKEGLKRIRDAGF V I DPDDVLPD	
		451-----500	
gls (2247)	(429)	FMFSDDGTICKERV-----	
GLSA_CORGL	(401)	FMFSDDGTICKERV-----	
GLSA_COREF	(406)	FDSDGTIKSPQVDDPEEL-----	
GLSA1_BRAJA	(429)	INTLREWTAEINVRDFYLLDTAIEWAEDQIVYRYGGSIDFHETTELAEQ	
GLSA2_BRAJA	(440)	MAAIAARTGDPPRLRRFALLDDAIEWAEDQVIYRFGGFTDVKESVHLGEQ	
GLSA_ANASP	(335)	-----	
Consensus	(451)	F FSDGT R-----	
		501-----550	
gls (2247)	(442)	-----	
GLSA_CORGL	(414)	-----	
GLSA_COREF	(424)	-----	
GLSA1_BRAJA	(479)	PLLEGLSADELAELGAICTIRTYQSGAKILTTGDPADALFFLRSGAVHVT	
GLSA2_BRAJA	(490)	ALLAELDTDEIAAIVKLSTTRHYTAGQRVI AAGAPANSLFFLQSGMVSVK	
GLSA_ANASP	(335)	-----	
Consensus	(501)	-----	
		551-----600	
gls (2247)	(442)	-----	
GLSA_CORGL	(414)	-----	
GLSA_COREF	(424)	-----	
GLSA1_BRAJA	(529)	LPDGVRLATLTAGMAFGEMALLEQTRSADVFADMAATAFEAPLKDFERFR	
GLSA2_BRAJA	(540)	LRSGVRLASLPGMEFGEMAILERTRSADVFADTPVACLELPLDSFADYR	
GLSA_ANASP	(335)	-----	
Consensus	(551)	-----	
		601-----635	
gls (2247)	(442)	-----	
GLSA_CORGL	(414)	-----	
GLSA_COREF	(424)	-----	
GLSA1_BRAJA	(579)	EQHPRASERIMRNLAQLLADRLIVANAKVDILTST	
GLSA2_BRAJA	(590)	RLHPETALKIMRNLAAILARRLVAANAKVDLLSAY	
GLSA_ANASP	(335)	-----	
Consensus	(601)	-----	

GLSA_CORGL : Q8NMT3: Corynebacterium glutamicum
 GLSA_COREF : Q8FMX4: Corynebacterium efficiens.
 GLSA1_BRAJA : Q89NA7: Bradyrhizobium japonicum,
 GLSA2_BRAJA : Q89KV2: Bradyrhizobium japonicum
 GLSA_ANASP : Q8YSZ5: Anabaena sp. (strain PCC 7120)

EXHIBIT B

Alignment of nucleotide sequences of glutamine synthetase genes

		1		50
2247	(1)	-----GTGGCGTTTGA-ACCCCGGAAGAAATTGTCAAGTT		
13032	(1)	-----GTGGCGTTTGA-ACCCCGGAAGAAATTGTCAAGTT		
CEfInA1	(1)	-----GTGGCGTTTAA-ACCCCGGAAGAAATTGTCAAGTT		
CEfInA2	(1)	-----GTGGCCTCGAGCCCGACAAACCCCGGATGAGATCCTCAAGTT		
MtugInA2	(1)	-----ATGGACCGACAGAAAGAAATTCGTTCCTCG		
MtugInA3	(1)	-----ATGACAGCCACACCGCTTCCCGCGCCCGCAT		
MtugInA4	(1)	GTGACCGGCCCCGGTTCCCGCCGTTGGCGTGCACCGAGTTGGAGCGACT		
MtugInA1	(1)	-----GTGACCGAAAG-ACCCCGACGACGTCTTCAAACT		
Consensus	(1)	GTGGCGGATGA ACCCGGA GAA T GTCAAGTT		
		51		100
2247	(36)	CATCA-AGGATGAA-AACGTGAGTTCGTTGACGTTCGATTCACCG		
13032	(36)	CATCA-AGGATGAA-AACGTGAGTTCGTTGACGTTCGATTCACCG		
CEfInA1	(36)	CATCA-AGGATGAA-AACGTGAGTTCGTTGACGTTCGATTCACCG		
CEfInA2	(45)	CATCC-GGGACAAT-GACATCAACTGGGTGGACGTCCAGTTCACCG		
MtugInA2	(30)	TACCC-TGGAGAACCGGACATCCGCTTCGTCCGGCTGTGGTTTCACAG		
MtugInA3	(33)	CGCCCAATTGGAGCGCAGAGGCGTGCACCGTCATCGGCACCGTCTGA		
MtugInA4	(51)	GGTCG-CGGCCGGT-GACGTGCACCGTCATCGTCCGCTTCACCG		
MtugInA1	(36)	TGCCA-AGGACGAG-AAGGTGCAATATGTGCACGTCCGGTTCTGTG		
Consensus	(51)	CATCA AGGA GAA GACGTGACTTCGTGCACGTCCGGTTCACCG		
		101		150
2247	(80)	ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT		
13032	(80)	ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT		
CEfInA1	(80)	ACCTTCCCGGCATCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT		
CEfInA2	(89)	ACGTTCCTCGGTTTCCTCAAGTCGGTCCGATCCGCCAGCGCACTTCGAC		
MtugInA2	(77)	ACGTCTCGGTTTCCTCAAGTCGGTCCGATCCGCCAGCGCACTTCGAC		
MtugInA3	(83)	ACCCCGCGGCACTCACCAGGCGAAGACCGTCCGATACGCCGAGCAAA		
MtugInA4	(95)	ACATCCAGGGC-----CGGCTGGCCGCAAAACGGATATCGGGCCGGCA		
MtugInA1	(80)	ACCTCCCTGGCATCATGCAGCACTTCAGCATTCGGCTTCGGCTTCGAC		
Consensus	(101)	ACCTTCCCGGCATCGAGCAGCACTTCAGCATCCC GCAGCCGGCTTCGA		
		151		200
2247	(130)	GCAGATACAGTCGAAGAAGTCTCGCATTCGACCGATCCTCGATCCGTGG		
13032	(130)	GCAGATACAAATCGAAGAAGTCTCGCATTCGACCGATCCTCGATCCGTGG		
CEfInA1	(130)	GAGGACCGCATCGAGGAGGGCTCGCTTCGACGGTTCCTCATCCGTGG		
CEfInA2	(139)	GAATCCGCATGAAAAACGACTGCGCTTCGACGGTTCATCGATCAGCGG		
MtugInA2	(126)	-----GGCGGCTTCGAGGAAGGCATCGGCTTCGACCGATCCTCGATCAGCGG		
MtugInA3	(132)	-----CAGATTCGCCAA-TCCGTGCGCT-CGGCGCCAGTCCGCTGTGCA		
MtugInA4	(138)	-----T-TTCGTGACGACATAGCCACCCGGGCGTGGAGTCTTCAG		
MtugInA1	(130)	AAGAGCGTGTTCGACGACGGCTTGGCTTTCGACGGTCTGTTCGATTCGCGG		
Consensus	(151)	G G CGC TTCGA GA GGCCTGCGCTTCGACGG TCCTCGATCCG GG		
		201		250
2247	(180)	CTTACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC-GGA		
13032	(180)	CTTACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC-GGA		
CEfInA1	(180)	TTTACCACCAATGATGAATCCGACATGAACCTGCTGCCAGATCTG-CCC		
CEfInA2	(189)	ATACACCACTGTCGACGATTCGGACATGATGCTGCTGCCAGATCTG-TCC		
MtugInA2	(174)	CTTTCGGCGGCTCTCGAATCCGATACGGTGGGGACCCCGAC-----		
MtugInA3	(174)	TACCTTCTGTATCGACCAATCGAGTATTCATTCACCGACACATCATG		
MtugInA4	(180)	TTATCTGCTGGCGTGGAGCTCGACCTGAACACGGTCCCGGGTAT-CCG		
MtugInA1	(180)	GTTCAGTTCGATCCACGAATCCGACATGTTGCTTCTTCGCGATCCC-GAG		
Consensus	(201)	TTCACCAGATCGACGAATCCGACATGAA CTGCTGCC GACCTC G		
		251		300

2247	(229)	ACGGCCACCCTTGATCC--ATTCGGCA--GGCAAGACCCTGAACGT
13032	(229)	ACGGCCACCCTTGATCC--ATTCGGCA--GGCAAGACCCTGAACGT
CEfInA1	(229)	ACGGCGAAGATCGATCC--GTTCGGCA--GGCGAAGACCCTGAACAT
CEfInA2	(238)	ACGGCGTTCATCGACCC--GTTCGGCAG--GTGGAAGACGCTCAACAT
MtugInA2	(218)	-CGTCGACCTTCAGGT--GCTGCCCTG--GGCCA--CC--
MtugInA3	(224)	TGGTCGGCGATCAACGT--CTCCGCAT--CGA--TC--
MtugInA4	(229)	ATGGCCAGTTGGGACACCGCTACGGCGATATGGTGAAGACGCGGACTT
MtugInA1	(229)	ACGGCGCCATCGACCC--GTTCGGGC--GGCAAGACGCTGAATAT
Consensus	(251)	ACGGCGACCATCGACCC GTTCGGCA GGCGAAGACCCTGAAC T
		301 350
2247	(273)	-TAAGTTCTTCGTTACGATCCCTTCACCCCGAGGGCA TTCTCCCGGGAC
13032	(273)	-TAAGTTCTTCGTTACGATCCCTTCACCCCGAGGGCA TTCTCCCGGGAC
CEfInA1	(273)	-CAAGTTCTTCGTTCCATGACCCCTTCACCCGTGAGGGCTTCTCCCGGGAC
CEfInA2	(282)	-CAAGTTCTTCGTTCCATGACCCCTATACCCGGGAACCATTTTCCCGGGAT
MtugInA2	(250)	-AGTTC--CGGCCACCACCACT--CAGCGCGGATGTTTGGGACATCA--
MtugInA3	(254)	-T--GTCCGCCCTTGGCCATCATGGGAGCGGGTTGGCGTG--GGCGCCCG
MtugInA4	(279)	GTCCACTCTGCGGCTGATTCCTTGGCTACCCGGGAACGGCGGTGGTATCG
MtugInA1	(273)	-CAACTTCTTTGTGCACGACCCCTTCACCCGTGAGCGGTACTCCCGCGAC
Consensus	(301)	TAAGTTCTTCGTTCCACGACCCCTTCACCCGGGAGGGCTTCTCCCGGGAC
		351 400
2247	(322)	CCACGCAACGTAGCAAGCAAGGCAGAGCAGTACCTGGC--ATCCACCGG
13032	(322)	CCACGCAACGTAGCAAGCAAGGCAGAGCAGTACCTGGC--ATCCACCGG
CEfInA1	(322)	CCCGCAATGTGGCAAGTAAGGCGAGCAGTCTCTGGC--CTCCACCGG
CEfInA2	(331)	CCCGCAACATCGCCCGCAAGGCGGAGGAGTACCTGGC--TTCCACCGG
MtugInA2	(293)	CCATGCCCGGACGGCTCGCC--GTCTGGGCGGACCCG--CGGCACGTG
MtugInA3	(299)	CGGGTTCTTTCAGCAGGACGGCACACCGGTCCCGGC--CTGCAGGCG
MtugInA4	(329)	CGGACCTGGTCTGGGCGGACGGCAGCGAGGTCCGCGTCTCGGCGGCGAGC
MtugInA1	(322)	CCCGCAACATCGCCCGCAAGGCGGAGAACTACCTGAT--CAGCACTGG
Consensus	(351)	CC CGCAAC TGGC CGCAAGGCAGAGCAGTACCTGGC CTGCACCGG
		401 450
2247	(369)	CATTGGCAGACACCTGCAACTTCGGCGCCGAGGCTGAGTTCTACCTCTTCG
13032	(369)	CATTGGCAGACACCTGCAACTTCGGCGCCGAGGCTGAGTTCTACCTCTTCG
CEfInA1	(369)	CATCGCGACACCTGCAACTTCGGCGCCGAGGCGGAGTTCTATCTCTTCG
CEfInA2	(378)	TTTCGGCGACAGCTGTAACTTCGGCGCCGAAGCCGAGTTCTACATCTTCG
MtugInA2	(337)	TTGGCGCGGACCTG--ACGAAGGC--C--GGC--GAACCTCGGTTCTCTCT
MtugInA3	(345)	AGGAACACTGAGCCGGATCGAGCCCGGCTTGGTGATGCCGGCATCGACG
MtugInA4	(379)	ATTCTGCGCGTCAAGCTCGATCGGCT--CAAGGC--GCGCGGACTGGTCCG
MtugInA1	(369)	CATCGCGACACCGCATACTTCGGCGCCGAGGCGGAGTTCTACATTTTCG
Consensus	(401)	CATCGCGACACCTGCAACTTCGGCGCCGAGGC GAGTTCTACCTCTTCG
		451 500
2247	(419)	ACTCCGTTTCGCTACTCCACCGAGATGAAC TCCGGCTTCTACGAAGTAGAT
13032	(419)	ACTCCGTTTCGCTACTCCACCGAGATGAAC TCCGGCTTCTACGAAGTAGAT
CEfInA1	(419)	ACTCCGTTCCGTTTACTCCACCGACATCAACTCCGGT TTCTACCATGTGGAC
CEfInA2	(428)	ACTCCGTTCCGTTTACGTTCCAGTCCAATCCGGCATTCACAGAGGTGGAT
MtugInA2	(380)	GGTACGTGCATCCCGAATCGAG--TTCTTCTGCTCAAG
MtugInA3	(395)	CGGTAATCGGCCACGAAGTCGA--TTCTCTTTGGTCGAC
MtugInA4	(425)	CCGATGTGGCACCGAGCTGGAGTTCACTGT--TTCCGACAGCGGTAT
MtugInA1	(419)	ATTCCGTGAGCTTCGACTGCGCGCCAACGGCTCTTCTACGAGGTGGAC
Consensus	(451)	ACTCCGTTCCGCTACGACACCGAG TCAAC CCG TTCTACGAGGTGGAT
		501 550
2247	(469)	ACCGAAGAAAGGCTGGTGGAAACCGTGGCAAGGAACCAACCTCGACGGAAC

13032	(469)	ACCGAAGAGGGCTGGTGGAAACCGTGGCAAGGAACCAACCTCGACGGCAG
CEFlnA1	(469)	ACCAACGAGGGTTGGTGGAAACCGTGGCCGTGAGACCAACCTCGATGGCAG
CEFlnA2	(478)	TCCGTGAGGGGCTGGTGGAAAGTGGTTCCCGGGAGAACCCGACGGCAG
MtuglnA2	(418)	CCC-----GGACCCGAGGACGG-----TCGGTCCCG
MtuglnA3	(433)	GCGGA-----C-----G-GCCAGCGGTGCCT-----TCGACG-CTG
MtuglnA4	(472)	CGCC-----AGGCA-----TGGCCAGCGG-----GTA-----TCGCGGGCTG
MtuglnA1	(469)	GCCATCTCGGGGTGGTGGAAACCGGGCGGGCGACCGAGGCCGACGGCAG
Consensus	(501)	CCGA GAGGGCTGGTGGAAACCGTGGC GGA ACCAACCTCGACGGCAG
		551 600
2247	(519)	CCGAACCTGGGCGCAAGAACCGCGTCAAGGGTGGCTACTTCCCAGTAG
13032	(519)	CCGAACCTGGGCGCAAGAACCGCGTCAAGGGTGGCTACTTCCCAGTAG
CEFlnA1	(519)	CCCCAACCCGGTTCCAAGAACCGCGTCAAGGGCGGTACTTCCCAGTCC
CEFlnA2	(528)	CAGGAACCTGGGTCAACAGGTACGGCAGAAAGGTGGTACTTCCCAGTGG
MtuglnA2	(446)	TCCC-----GGTCG-A-----CAACGGCGGCTATTTCGACCAAG
MtuglnA3	(463)	T-----GGGC-----GC-----AGTACGG-----TGTCGGCGGG
MtuglnA4	(505)	ACCC-----C-GGGC-----AGCGA-----GTACAACATCGACTACGGATATTGG
MtuglnA1	(519)	TCCCAACCGGGGTACAAGGTCCGCCACAAGGGCGGGTATTTCGAGTGG
Consensus	(551)	CCCCAAC GGGCC AAG CCGC CAAGGGCGGCTACTTCCCAGTGG
		601 650
2247	(569)	CA-CCATACGACCAAACCGTGGACGTGGCGGATGACATGGTTCGCAACC
13032	(569)	CA-CCATACGACCAAACCGTGGACGTGGCGGATGACATGGTTCGCAACC
CEFlnA1	(569)	CA-CCCTACGACCAAGACCGTGGACGTGGCGGATGACATGGTTCGCAACC
CEFlnA2	(578)	CA-CCCTATGACCACTTCCAGGACGTGGCGGACACCATTTGGTGGACCC
MtuglnA2	(479)	CG-GTGCACGACTCCGCTTGAACTTTCGGCGCCACGGCATCGATGCC
MtuglnA3	(488)	TG-CTCGAGCAGAGGGCTTCG-TCCGGATGTCAACCGCGGGCAA
MtuglnA4	(545)	CATCCTGGCGATGCAGCCGTTC-CTGGCGACATCCGTTGGGTAA
MtuglnA1	(569)	CC-CCCAACGACCAATACGTGGACGTGGCGGACAGATGCTGACCAACC
Consensus	(601)	CA CCCTACGACCAA CCGT GAC TGGCGATGACATGGT GGCAACC
		651 700
2247	(617)	TCCAGCTTCCGGCTTCGGTCTTGAGCGTTTCCACCAGGAAGTCGG-T
13032	(617)	TCCAGCTTCCGGCTTCGGTCTTGAGCGTTTCCACCAGGAAGTCGG-T
CEFlnA1	(617)	TCCGTGACGCGGGTTCCACCTGGAGGGTTTCCACCAGGAGTCGG-T
CEFlnA2	(626)	TGGCGAGATCGGGTTCCACCTGGAGCGTTCCACCATGAGATGGCAGT
MtuglnA2	(527)	TGCAATTATGGGATCTCGGTGGAGTTCAGCCATCAGGAAGGGC-A
MtuglnA3	(533)	CGGCAG-----CAGGATCGCTATCGAGCAGTCCATCCCGAATACGG-T
MtuglnA4	(590)	TGGCCGGTGGGGTCTGGGATTCGAGCGCGTCAAGGCGAATGCAA-C
MtuglnA1	(617)	TGATCAACTCCGGCTTCATCTGGAGAAGGGCCACCAGGAGTGGGCAGC
Consensus	(651)	TGGCAG CCGGCTTC C CTGGAGCGTTTCCACCAGGAAGTCGG T
		701 750
2247	(664)	GGCGGACAGCAGGAATCAACTACCGTTCAACACCATGCTCCAGCGGGC
13032	(664)	GGCGGACAGCAGGAATCAACTACCGTTCAACACCATGCTCCAGCGGGC
CEFlnA1	(664)	GGCGGCGAGCAGGAGATCAACTACCGTTCAACACCGCTCTGCACGAGC
CEFlnA2	(676)	GGTGGTCAGCAGGAGATCAACTACCGTTCAACACCGCTGCTCGCGCAGC
MtuglnA2	(574)	CCCGGCGAGCAGGAGATCGACTGCGGTTCGGGAGCGCTCTGTCGATGGC
MtuglnA3	(577)	GCGAACCAATTGAGATCTCGTTAGCGCGCGAGCGCGGGTCGGGCCGC
MtuglnA4	(637)	ATGGGCGAGCAGGAGATCGGGTTTCGTTACGAGAGGGCGCTGGTACCTG
MtuglnA1	(667)	GGCGGACAGGCCGAGATCAACTACCGTTCAATTTCGGTGGTGCACGCCGC
Consensus	(701)	GGCGGCGAGCAGGAGATCAACTACCG TTCAACACCGTCTGTCACGC GC
		751 800
2247	(714)	AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGCCTCC
13032	(714)	AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGCCTCC

CEfInA1	(714)	CGATGACATTCAGACCTTCAAGTACATCGTGAAGAACACCGCAGCCCTGC
CEfInA2	(726)	CGATGACCTCCAGACCTTCAAGTACGTTGGTGAAGAACACCGCGAAGGCCG
MtugInA2	(624)	TGACAACGTGATGACCTTCGGCTACGTCATCAAAGAAGTCGGCTGGAAG
MtugInA3	(627)	CGATCAGCTGGTGCTGACCCGGCTCATCATCGCCGTACCGCCGGCCGGC
MtugInA4	(687)	CGACAACCATGCGATCTACAAGAAGGGCGCAAGGAAATCGCCGACCAAGC
MtugInA1	(717)	CGACGACATGCAGTTGTACAAGTACATCATCAAGAACACCGCTGGCAGA
Consensus	(751)	CGATGACAT CAGACCTTCAAGTACATCATCAAGAACACCGC CGCC GC
		801 850
2247	(764)	ACGGCAAGGCTGCAACCTTCATGGCTAAGCCACTGGCTGGCGACAACGGT
13032	(764)	ACGGCAAGGCTGCAACCTTCATGGCTAAGCCACTGGCTGGCGACAACGGT
CEfInA1	(764)	ACGGCAAGGCTGCCACCTTCATGCCAAGCGCTGGCCGGTGACAACGGC
CEfInA2	(776)	TCCGTAATCCGCCACCTTCATGCCAAGCGCTGGCTGATGACGGGGT
MtugInA2	(674)	AGGGCGCCCGGGCGTCTTCATGCCAAGCCATTCGGCCAGCACCCGGG
MtugInA3	(677)	ACGGGTTACGGGTGACCTATCGCCAGCGCCCTTCGGCGGAAGTATCGGA
MtugInA4	(737)	ACGGCAAGAGCCTAACCTTCATGCGGAAATACGATGAACCGGAAGGT
MtugInA1	(767)	ACGGCAAAAGGTCACCTTCATGCCAAGCGCTGTTCCGGCGACAACGGG
Consensus	(801)	ACGGCAAG C GC ACCTTCATGCCAAGCCACTGGCTGG GACAACGGT
		851 900
2247	(814)	TCCGGCATGCAGGCTGACCAGTCCCTTGGAAGGACGGCAAGCCACT
13032	(814)	TCCGGCATGCAGGCTGACCAGTCCCTTGGAAGGACGGCAAGCCACT
CEfInA1	(814)	TCCGGCATGCAGGCGCCAGCAGTCCCTTGGAAGGACGGCAAGCCACT
CEfInA2	(826)	TCCGGCATGCACATCCACCAGTCCGTGGAAGGACGGCAAGCCCTT
MtugInA2	(724)	TCCGGCATGCACACCCACATGAGCCTGTTGAGGGTGATGTCAACCGGT
MtugInA3	(727)	TCCGGTGCCACCAACACTTCGCGTCACTATGTGGGAAGGATGCT
MtugInA4	(784)	AATAGCTGTACATCCATGTCGCGTCCGTGGCAGGATGGCTCCCGGT
MtugInA1	(817)	TCCGGCATGCAGTGTCACTGCGTGTGGAAGGACGGGGCCCGCT
Consensus	(851)	TCCGGCATGCAC CCCACCAGTCCGTGGAAGGACGGCAAGCCGCT
		901 950
2247	(861)	CTTCCACGATGA GTCCGGCTACGCAAGGCTGTCCGACATCGCCCGCTAC
13032	(861)	CTTCCACGATGA GTCCGGCTACGCAAGGCTGTCCGACATCGCCCGCTAC
CEfInA1	(861)	CTTCCACGACGA GTCCGGCTACGCCGGCTGTCCGACATCGCCCGTTAC
CEfInA2	(873)	CTTCCATGATGA GCGCCGTTATGCCAAGCTGTCCGGATGGCCCGTAC
MtugInA2	(774)	CCACAGCGCTGATGATCCGCTGCAGCTGTGGGAAGTGGGTAATCG
MtugInA3	(774)	GTCTCCGGTGGGACTGGAGCAGGTGGCATGACCTCGGCCGGGAGGCC
MtugInA4	(834)	GTTTGGCGACAGTAACGGCCCGCACCGCATGTGCTCGATGTCCCGACG
MtugInA1	(864)	GATGTACGACGA GACGGGTTATGCCGGTCTGTGGGACACGGCCCGTCA
Consensus	(901)	CTTCCACGATGA GACCGGCTACGC GGCCTGTCCGACATGGCCCG TAC
		951 1000
2247	(910)	TACATCGGCGGCATCCTGCACCACGCAAGGCGGTGTTCTGGCGTT-CACCA
13032	(910)	TACATCGGCGGCATCCTGCACCACGCAAGGCGGTGTTCTGGCGTT-CACCA
CEfInA1	(910)	TACATCGGTGGCATCCTGCACCACGCGGTGGGTCTGGCGTT-CACCA
CEfInA2	(922)	TATGTGGTGGTCTGCTCAAGCATGCCCGCGGTGTGGCTTT-CACCA
MtugInA2	(820)	TTCATCGCCGGGATCCTGGAGCAGGTTGGGAGATCAGCGCGGT-CACAA
MtugInA3	(823)	GCGGTGCAGGAGTGCCTGCGGACTACCGACGCCAAGGCATCCTGT
MtugInA4	(883)	TTCGTCCCGGCCAGTTGGCCACGTTGGCGGAATTCACGTTGTGTATG
MtugInA1	(913)	TACATCGGCGGCCTGTTACACCACGCGCCGTGCTGTGGCGTT-CACCA
Consensus	(951)	TACATCGGCGGCATGCTGCACCACGC GCGCGGT CTGGCGTT CACCA
		1001 1050
2247	(959)	ACGCCAACCTGAACCTCCTACCAACCGTCTGGTTCCAGGCTTCGAGGCTCCA
13032	(959)	ACGCCAACCTGAACCTCCTACCAACCGTCTGGTTCCAGGCTTCGAGGCTCCA
CEfInA1	(959)	ACCGGACCTGAACCTCCTACCATCGCTGGTGGCGGCTTCGAGGCCCC

CEFlnA2	(971)	ACCCGACCCTGAATTCCTACAACCGTCTGGTGGCGGGTTTCGAGGCCCGG
MtuglnA2	(869)	ATCAGTGGGTCAACTCTTACAAGCGGCTGGTGCAGGGCGGGAAGCGCC
MtuglnA3	(872)	GGGATCGATCGTGTCCGGTCTGGGAATCGCAACCGTAAGTGGCCGGA
MtuglnA4	(932)	CGCCGACCAATAACTCCTACAAGCGATTTCGGATAGCAGTTTCGCGCG
MtuglnA1	(962)	ACCCGACGGTGAACCTCTACAAGCGGCTGGTTCGCGGTTCGAGGCCCGG
Consensus	(1001)	ACCCGACCCTGAACCTCTACCAGG CTGGT CC GGCTTCGAGGCCCG
		1051 1100
2247	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTTCGGCTGGTGTCCGTATCCC
13032	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTTCGGCTGGTGTCCGTATCCC
CEFlnA1	(1009)	ATCAACCTGGTGTACTCCAGCGCAACCGTTCGGCGGCGGTGGGTATCCC
CEFlnA2	(1021)	GTGAGCCTGGCGTATTCGAGCGAAGACCGTTCGGCGGCGATCCGATTC
MtuglnA2	(919)	ACGGCGCGCTCGTGGGGGGCGGCAACCGATCCGGCCTAGTGGCGGTGG
MtuglnA3	(922)	ATCTATGCATGCTGGGGTACCGAAAACCGGGAAAGGGCGTGGCATTCGT
MtuglnA4	(982)	ACGGCGCTGGCTTGGGGGTGGACAAATCGACCTGCGCCCTGGCGGTG--
MtuglnA1	(1012)	ATCAACCTGGTCTATAGCAGCGCAACCGTTCGGCATGCGTGCGCATCCC
Consensus	(1051)	ATCAACCTGGTGTATG CAGCGCAACCG TCCGC GC GTGCG ATCCC
		1101 1150
2247	(1059)	AAT CACCGGATCCAACCGAAGGCAAGCGCATCGAATTCGGCGCTC
13032	(1059)	AAT CACCGGATCCAACCGAAGGCAAGCGCATCGAATTCGGCGCTC
CEFlnA1	(1059)	GAT CACCGGTTCCAACCGAAGGCAAGCGCATCGAGTTCGGCGCAC
CEFlnA2	(1071)	GGC CACCGGTTCCAACCGAAGGCAAGCGCATCGAGTTCGGCACCC
MtuglnA2	(969)	GATGTACACGGCGCAAGACCTCGTGGCGCGGGTCGAAGTACGACGG
MtuglnA3	(972)	CAAGGGCGGGCTGGCAGCGCGTACGGCGGGAAGTGGAGGTGAAGCTCG
MtuglnA4	(1030)	GTGGGCGACGGG CAAACAT C CGGGTCGAATGCCCGCTTC
MtuglnA1	(1062)	GAT CACCGGCAGCAACCGAAGGCAAGCGGCTCGAGTTCGGAAGCC
Consensus	(1101)	GAT CACCGG CCAACCGAAGGC AAGCGCATCGAGTTCGGCGCC
		1151 1200
2247	(1106)	CAGACCCATCAGGCAACCCATACCTGGGCTTCGCAAGCATGATGATGGCC
13032	(1106)	CAGACCCATCAGGCAACCCATACCTGGGCTTCGCAAGCATGATGATGGCC
CEFlnA1	(1106)	CGGACCCATCCGGCAACCCATACCTGGGCTTCGGCGGCATGATGATGGCC
CEFlnA2	(1118)	CGGACCCCTCGGGTAACCCATACCTGGGCTTCAGCGGCATGATGATGGCG
MtuglnA2	(1019)	CTGATTGGCGTGCATTCCTATCTGACATTCGCGGTCTGTGGCGGG
MtuglnA3	(1022)	TCGACCCGTCCGCCAACCCGATCTCGCGTCCGGCGGCATCTCGGACTG
MtuglnA4	(1070)	CCGGCGGTGATGTCAACCAATACCTGGCGGTGGCGGTCTCATTCGTGGA
MtuglnA1	(1109)	CCGACTCGTCGGGCAACCCGATCTCGCGGTCTCGGCCATGCTGATGGCA
Consensus	(1151)	C GACCC TCGGGCAACCC TACCTGGCGTTCGC GCGATGATGATGGC
		1201 1250
2247	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACAGGTCCAGTGGACAA
13032	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACAGGTCCAGTGGACAA
CEFlnA1	(1156)	GGCCTGGACGGTGTGAAGAACCGCATCGAGCCGACGGACCGGTGGACAA
CEFlnA2	(1168)	GGCCTGGACGGCATCGGCAACCGCATCGAACCAGCGCCCTCTGGACAA
MtuglnA2	(1069)	GGATTGCGGGGTGTAGAGAAGGTTACGTGCTGGGCCCGGAGCCGAGGA
MtuglnA3	(1072)	GCATTCGACGGCATGAAGACCAAGCGGTGTTGCGGTCCGAAACBACCGT
MtuglnA4	(1120)	GGGTTGTACGGTATCGAGCGGGGCTTCAGGTGCGCGAGCCCTGTCTGG
MtuglnA1	(1159)	GGCCTGGACGGTATCAAGAACAGATCGAGCCGCAAGGGCGCTCGACAA
Consensus	(1201)	GGCCTGGACGGTATCAAGAACCGCATCGAGCCGACGGGCC GTGGACAA
		1251 1300
2247	(1206)	GGACCTCTACGAATGCCACCAAGAGGCTGCATCCAT-----TCCAG
13032	(1206)	GGACCTCTACGAATGCCACCAAGAGGCTGCATCCAT-----TCCAG
CEFlnA1	(1206)	GGACCTCTACGAGCTCCACCGAGGAGGGCGGTCCAT-----CCCGC
CEFlnA2	(1218)	GGACCTCTATGAGGTCCGCCCGAGGAGGCTGCCAAGGT-----CGCCG

MtugInA2 (1119) CAACGTA TGGGACCTCA CACC CGAGGAACGCCGAGCGAT GGGGTACCGAG
 MtugInA3 (1122) AGACCGACACAGCTGTGTGACGTGGATCGTGACCGTGCCGGCATTGTGC
 MtugInA4 (1170) CAACG-----CCT ACC-----AAGCGCCGATGT-----CGAAC
 MtugInA1 (1209) GGATCTCTACGAGCTGCCGCCGAAAGAGCCCGAGTAT-----CCCGG
 Consensus (1251) GGACCTCTACGAGCT CCACC GAGGAAGCTGCC C AT CCCAC
 1301 1350
 2247 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC
 13032 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC
 CEFgInA1 (1250) AGGCACCGACCTCCCTGGAGGCATCCCTGAAGGCCCTGCAGGAAGACTCC
 CEFgInA2 (1262) AGGCCCCACCTCACTGGAACAGGCCCTGAAGGCCCTGGAGGAAGACAC
 MtugInA2 (1169) AATTGCCGTCCAGTTTGGATAGTCCGCTCCGCCCATGGAGGC-----CTCC
 MtugInA3 (1172) GACTTGCTGCCGATCAGGCCGATGCAATTGCTGTACTGGATAG-----TTCC
 MtugInA4 (1199) GCTGCCGTTTACGCTGCCGACGCCGCCGTCTGTTCGAGGA-----TTCT
 MtugInA1 (1253) AGACTCCGACCCAGCTGTAGATGTGATCGACCGTCTCGAGGCCGACAC
 Consensus (1301) AGGC CCGACCTC CTGGAAGA GCCCTGAAGGC CTGGAGGA GACTCC
 1351 1400
 2247 (1300) GACTTCCTCACCAGTCTGACGTCTTACCCGAGGATCTCATCGA GCGGT
 13032 (1300) GACTTCCTCACCAGTCTGACGTCTTACCCGAGGATCTCATCGA GCGGT
 CEFgInA1 (1300) GACTTCCTCACCAGTCCGACGTGTTACCCGAGGACCTCATCGA GCGGT
 CEFgInA2 (1312) GAGTTCCTCACCAGGGTGACGTGTTACCCGATCATCATCGA GCGGT
 MtugInA2 (1216) GAACTCGTCCCGAG-----GCCCTGGGGGAGCAGTTTTTGA CTTTT
 MtugInA3 (1218) GAAACTGCTTCGCTG-----CATCCTTGCCGATCCCGTGGTAGATGCGGT
 MtugInA4 (1246) GCGCTGGTGGCGAG-----GCCCTCGCGAGGATGTTGTCCG GCACT
 MtugInA1 (1303) GAATACCTCACCAGAGGAGGGGTGTTACAAACGACCTGATCGA GACGT
 Consensus (1351) GA TTCTCACCAG GACGTGTTACCGAGGATCTCATCGA GCGGT
 1401 1450
 2247 (1349) ACATCCAGTACAAGTAC-----GACAACGAGATCTCCCGAGTTCCGCTGCGC
 13032 (1349) ACATCCAGTACAAGTAC-----GACAACGAGATCTCCCGAGTTCCGCTGCGC
 CEFgInA1 (1349) ACATCCAGTACAAGTAC-----GACAACGAGATCAGCCCGGTCCGCTGCGC
 CEFgInA2 (1361) ATGTGCCCTACAAGCAT-----GAACATGAGATCAGCCGTGAGCGTCTGCGC
 MtugInA2 (1259) TCTTCCGCAACAAGCGCACGAGTGGGCGAACTACCGCAGCCACGTACG
 MtugInA3 (1263) GGTCCGGTACGCCAGT-TAGAGCATGAGCGCTAC-----GGTGACCTCGAT
 MtugInA4 (1289) AGCTGACAACGCCCGGTGTGAGCTGGCGGCGTTCAACGCGCGGTCA-----
 MtugInA1 (1352) GGATCAGTTTCAAGCGC-----GAAACGAGATCGAGCCGGTCAACATCCGG
 Consensus (1401) ACATGCAGTACAAGCGC GA AACGAGATCTCCCG GT CGCCTGCGC
 1451 1495
 2247 (1396) CCAACCCCGCAGGAATTGGAATTGTAAGTTCGACTGC-----
 13032 (1396) CCAACCCCGCAGGAATTGGAATTGTAAGTTCGACTGCCTAA-----
 CEFgInA1 (1396) CCCACCCCGCAGGAGTTGAGCTGTACTTCGACTGCTAG-----
 CEFgInA2 (1408) CCCACCCGTCTGGATTTCGAGCTGTACTTCGACTGCTAG-----
 MtugInA2 (1309) CCATACGAGCTGCGCACCTACCTGTCCGTGTAG-----
 MtugInA3 (1309) CCGTCCGAGCTGCCGACAAGTTCCGGATGGCTTCGAGTGTGTAA
 MtugInA4 (1337) CCGATTGGGAGAGGATACGTGGATTGAGCGCTCTAG-----
 MtugInA1 (1399) CCGCATCCCTACGAATCCGCTGTACTTCGACTGCTAA-----
 Consensus (1451) CC ACCCGCAGGAATTCGAGCTGTACTTCGACTGCTA

2247 : B. flavum ATCC14067

13032 : C. glutamicum ATCC13032

CEF: C. efficiens YS314

Mtu: Mycobacterium tuberculosis H37RV